Fig. 1

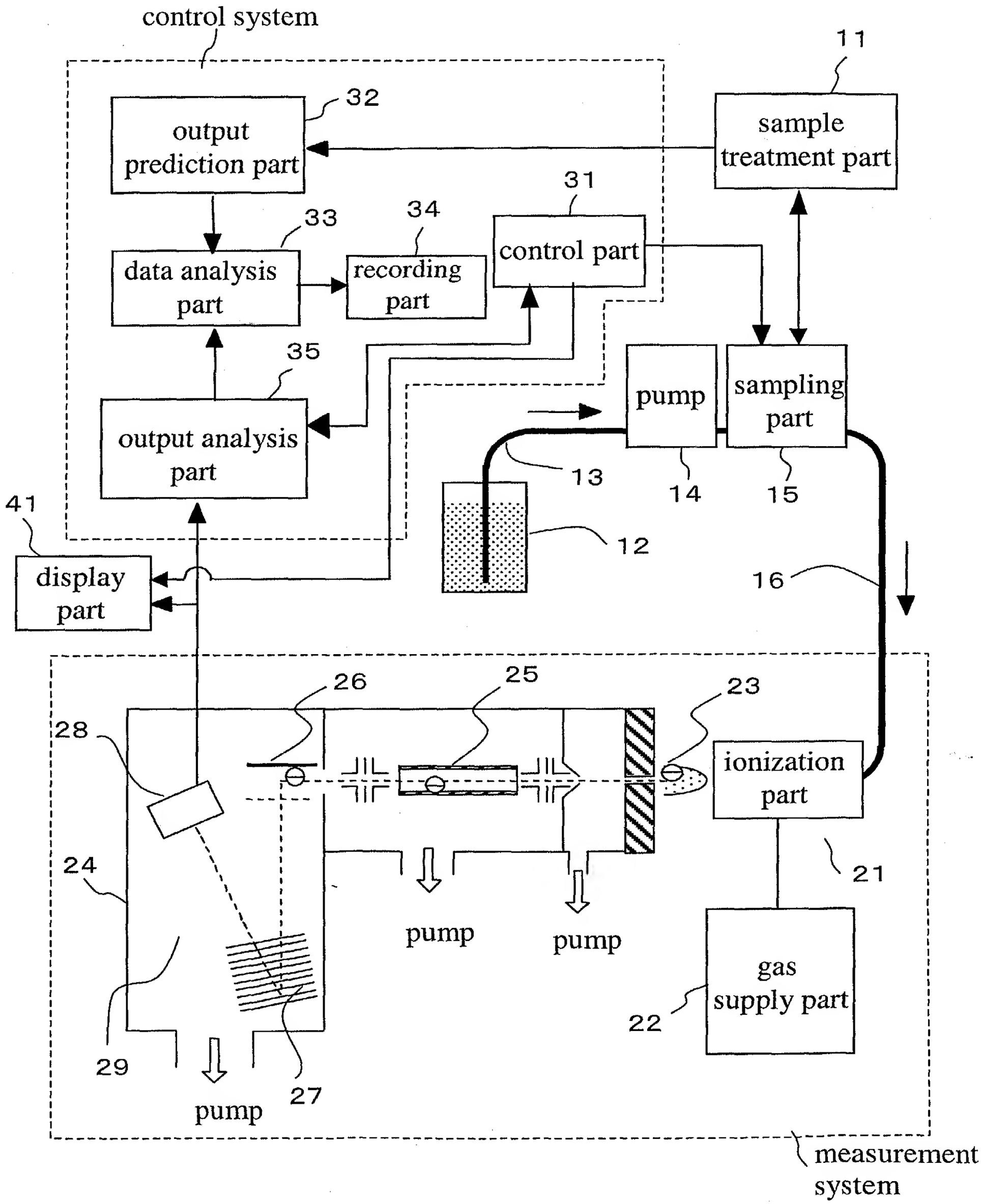
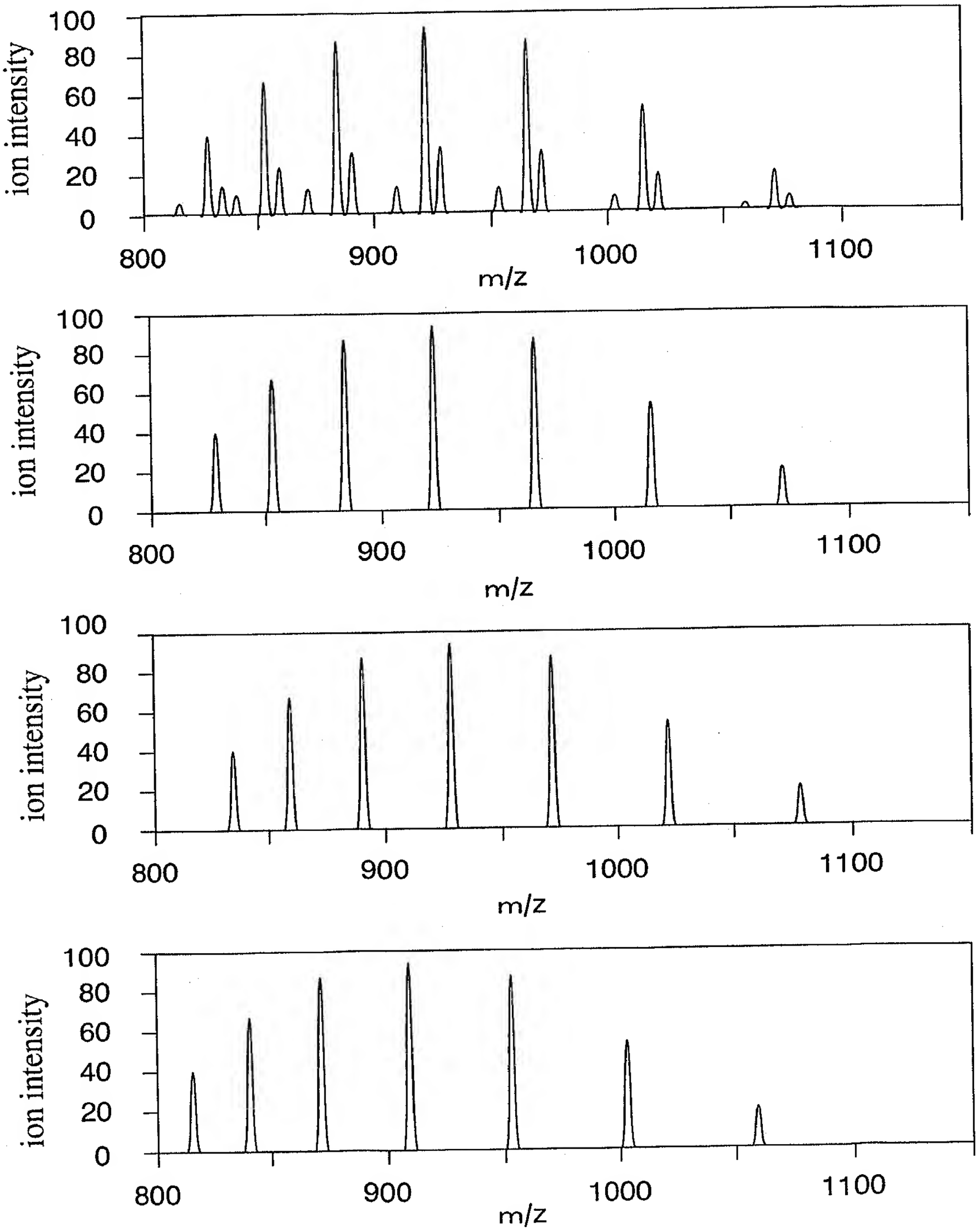

control system
11
32
output prediction part
sample treatment part
31
33
34
data analysis part
recording part
control part
35
output analysis part
pump
sampling part
13
14
15
41
display part
12
16
26
25
23
28
ionization part
24
21
pump
pump
gas supply part
22
29
27
pump
measurement system

Fig. 2

I(i)



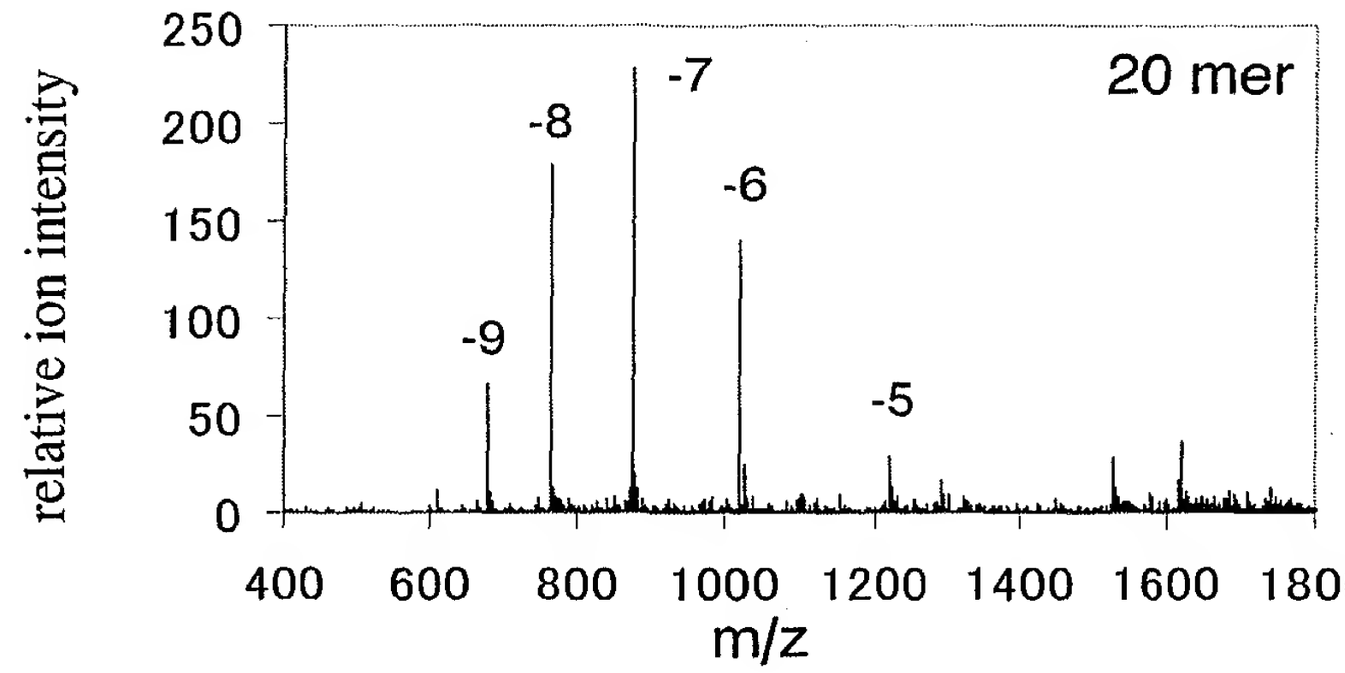
S(i)

S(i -1)

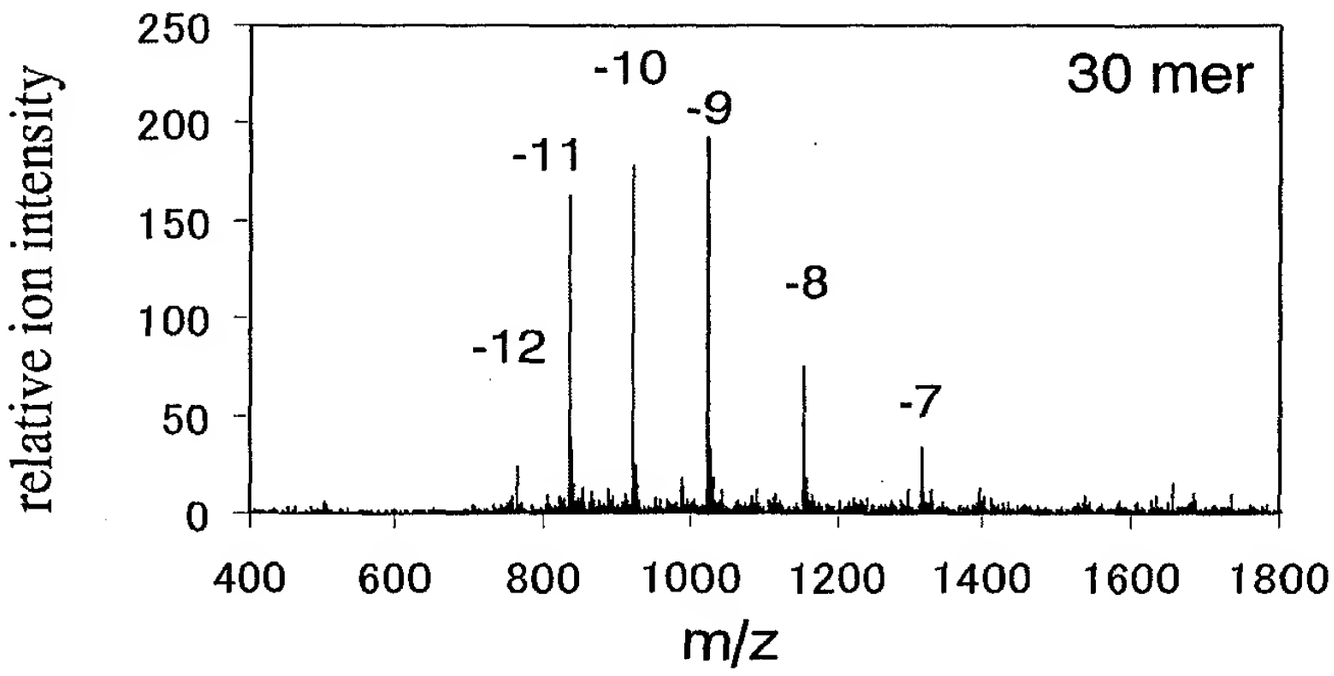
S(i -2)

Fig. 3

(a)


relative ion intensity
250
200
150
100
50
0
-9
-8
-7
-6
-5
20 mer
400
600
800
1000
1200
1400
1600
1800
m/z

(b)


relative ion intensity
250
200
150
100
50
0
-12
-11
-10
-9
-8
-7
30 mer
400
600
800
1000
1200
1400
1600
1800
m/z

(c)

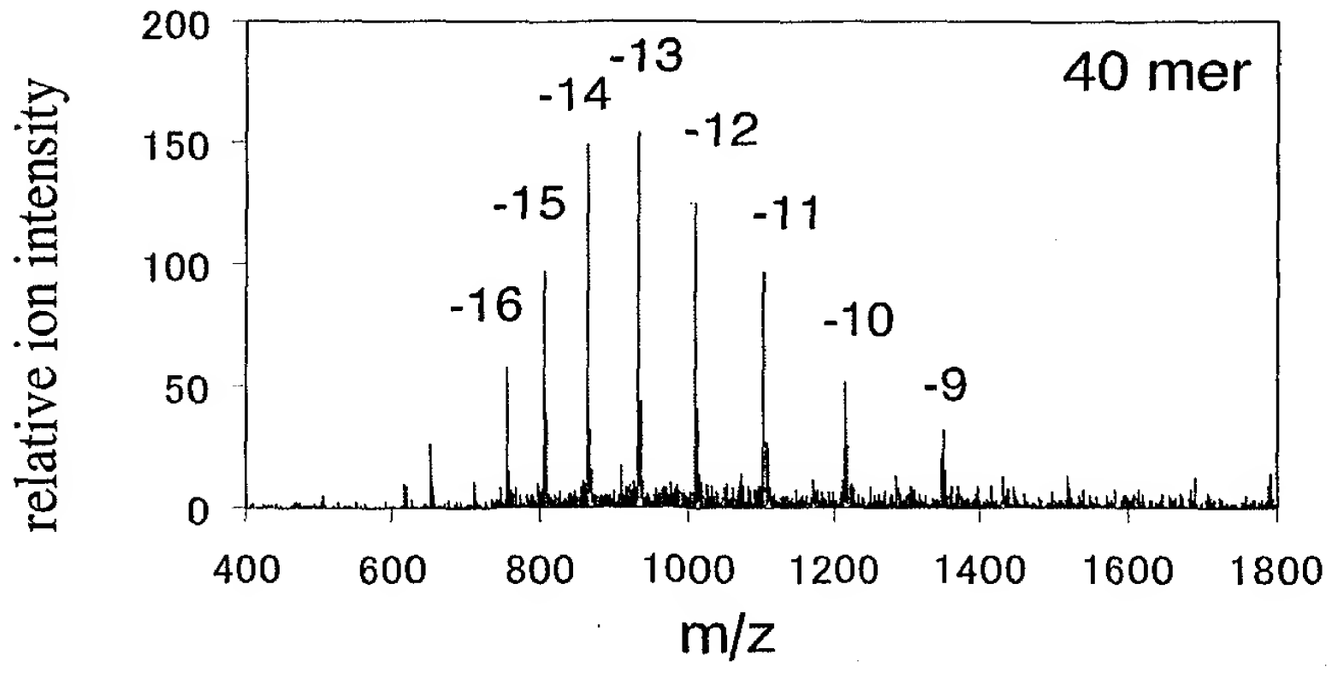

relative ion intensity
200
150
100
50
0
-16
-15
-14
-13
-12
-11
-10
-9
40 mer
400
600
800
1000
1200
1400
1600
1800
m/z

Fig. 4

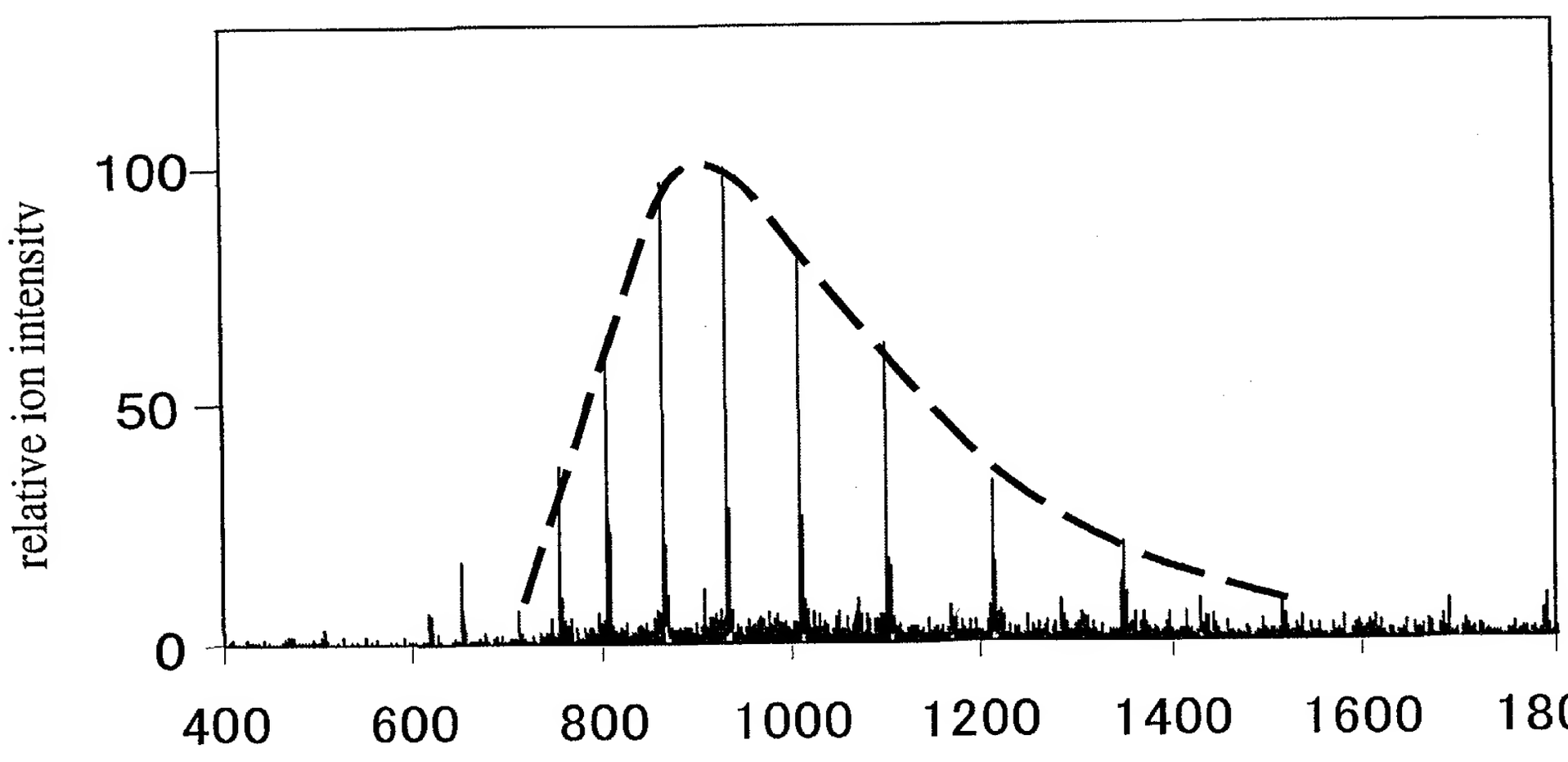
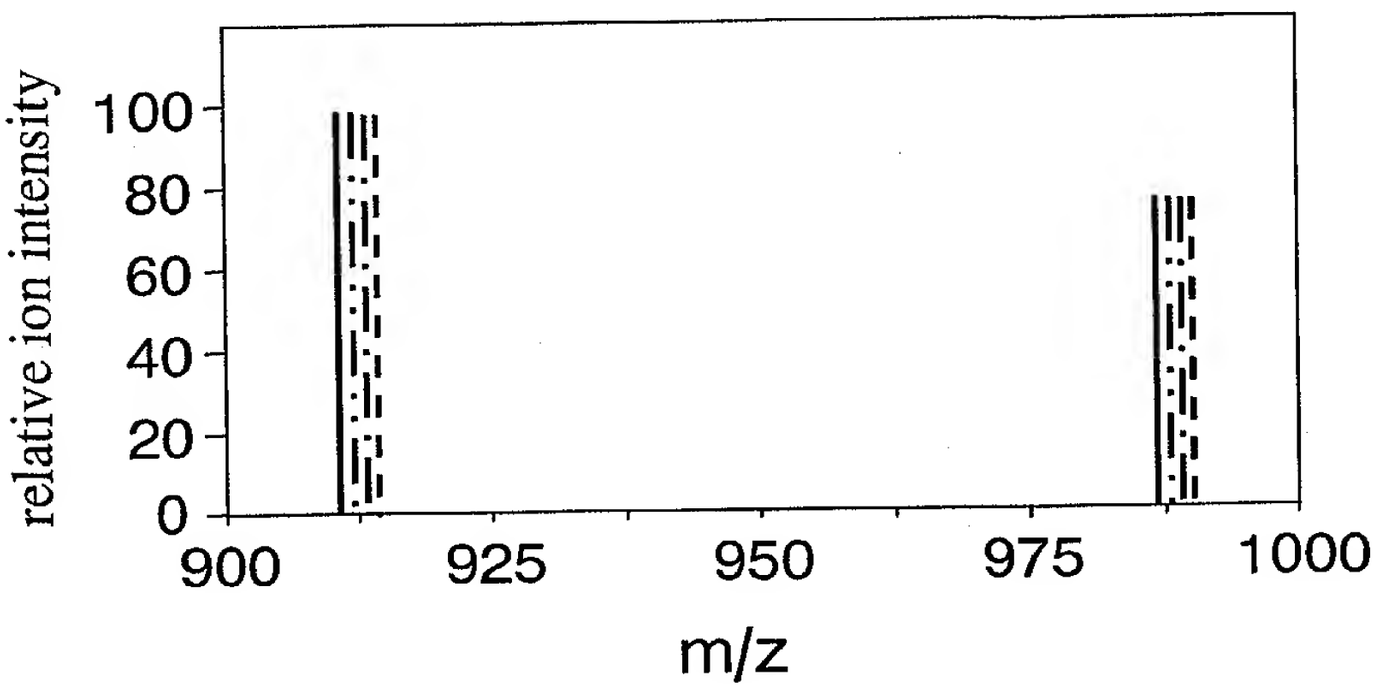
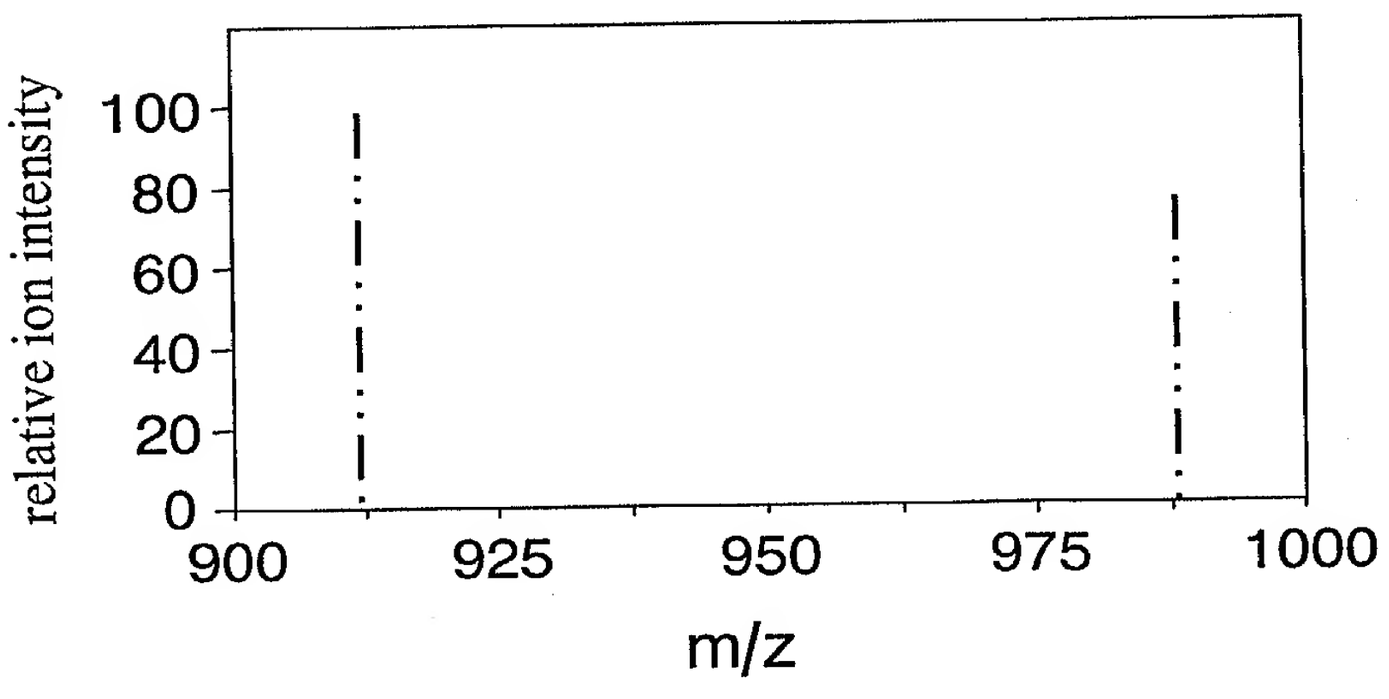

relative ion intensity
100
50
0
400
600
800
1000
1200
1400
1600
1800
m/z

Fig. 5

(a)


relative ion intensity
100
80
60
40
20
0
900
925
950
975
1000
m/z

(b)


relative ion intensity
100
80
60
40
20
0
900
925
950
975
1000
m/z

(c)

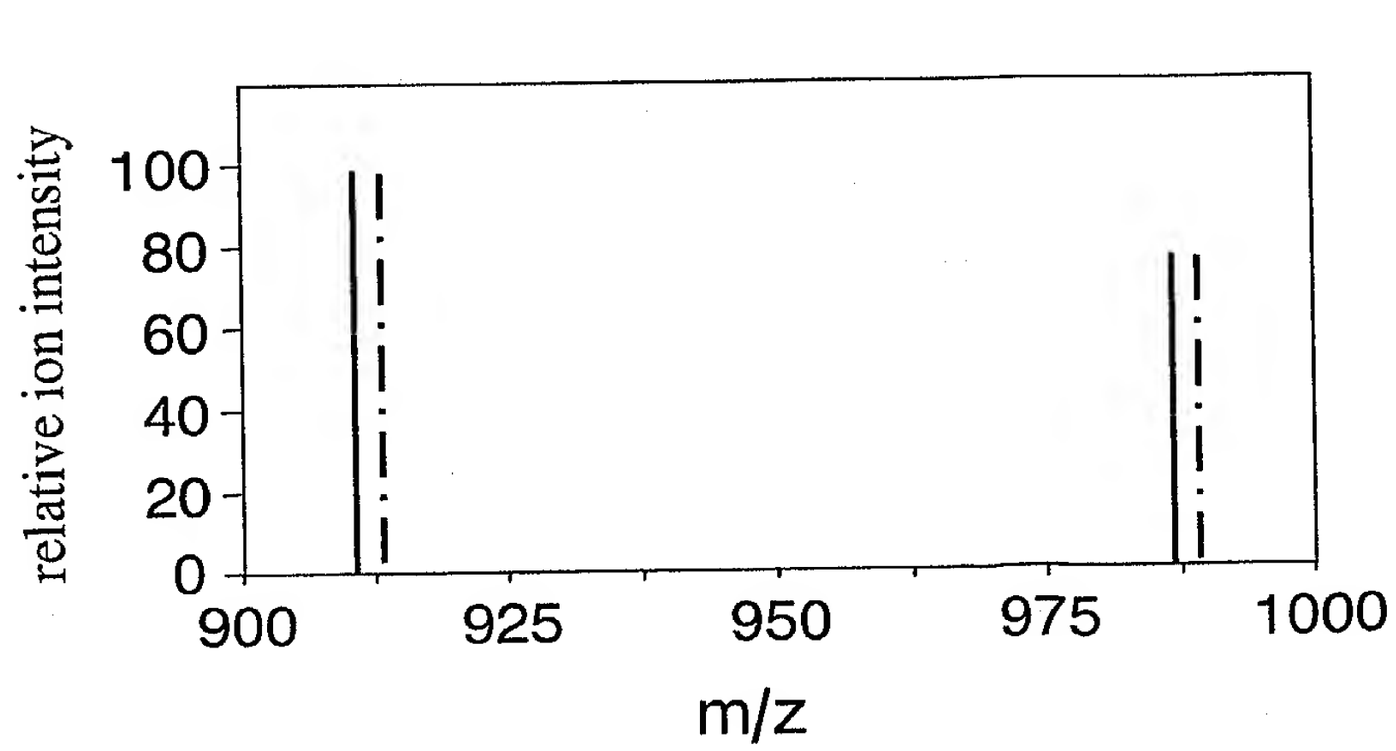

relative ion intensity
100
80
60
40
20
0
900
925
950
975
1000
m/z

Fig. 6

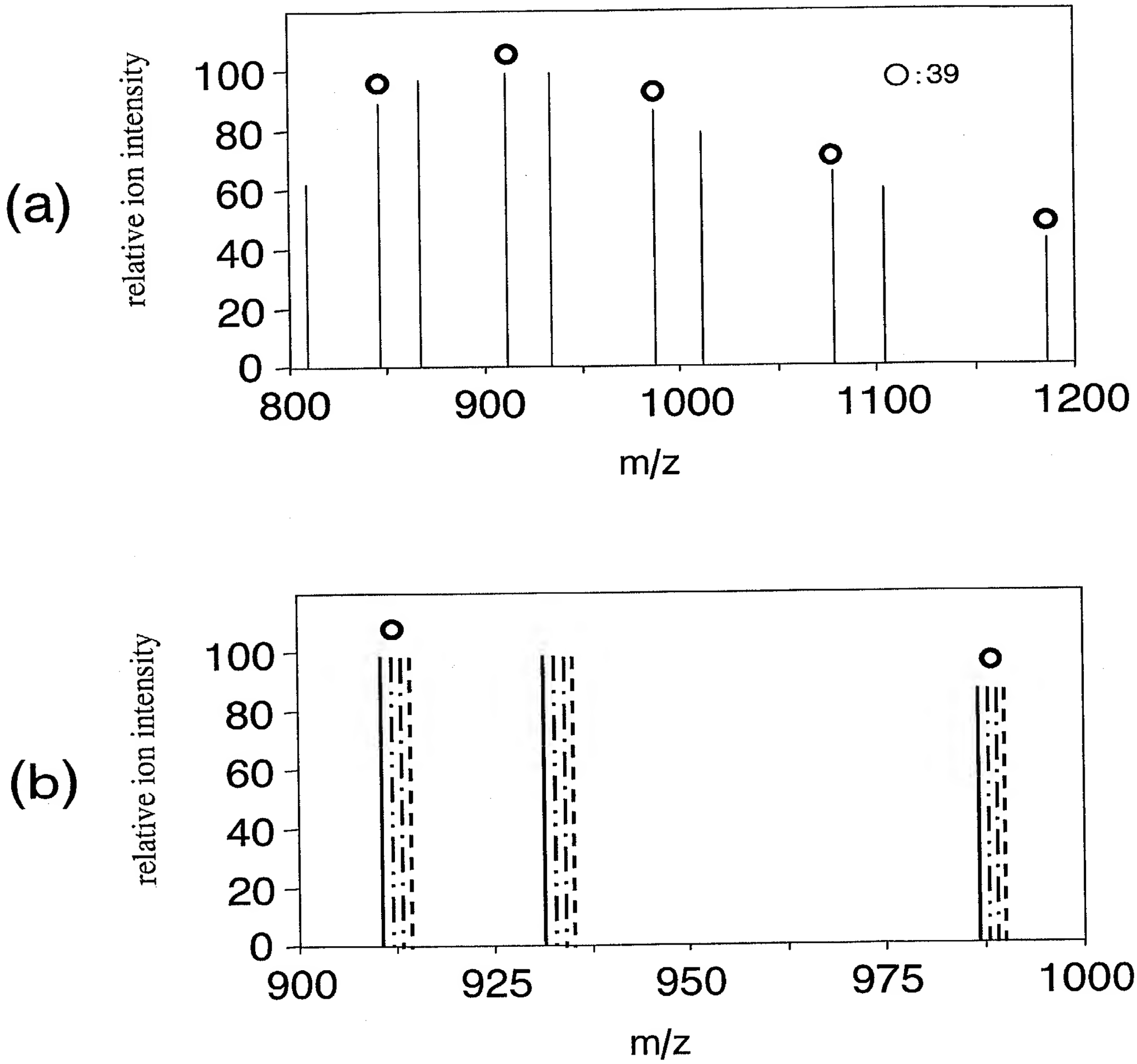

(a)
relative ion intensity
100
80
60
40
20
0
800
900
1000
1100
1200
m/z
○:39
(b)
relative ion intensity
100
80
60
40
20
0
900
925
950
975
1000
m/z

Fig. 7

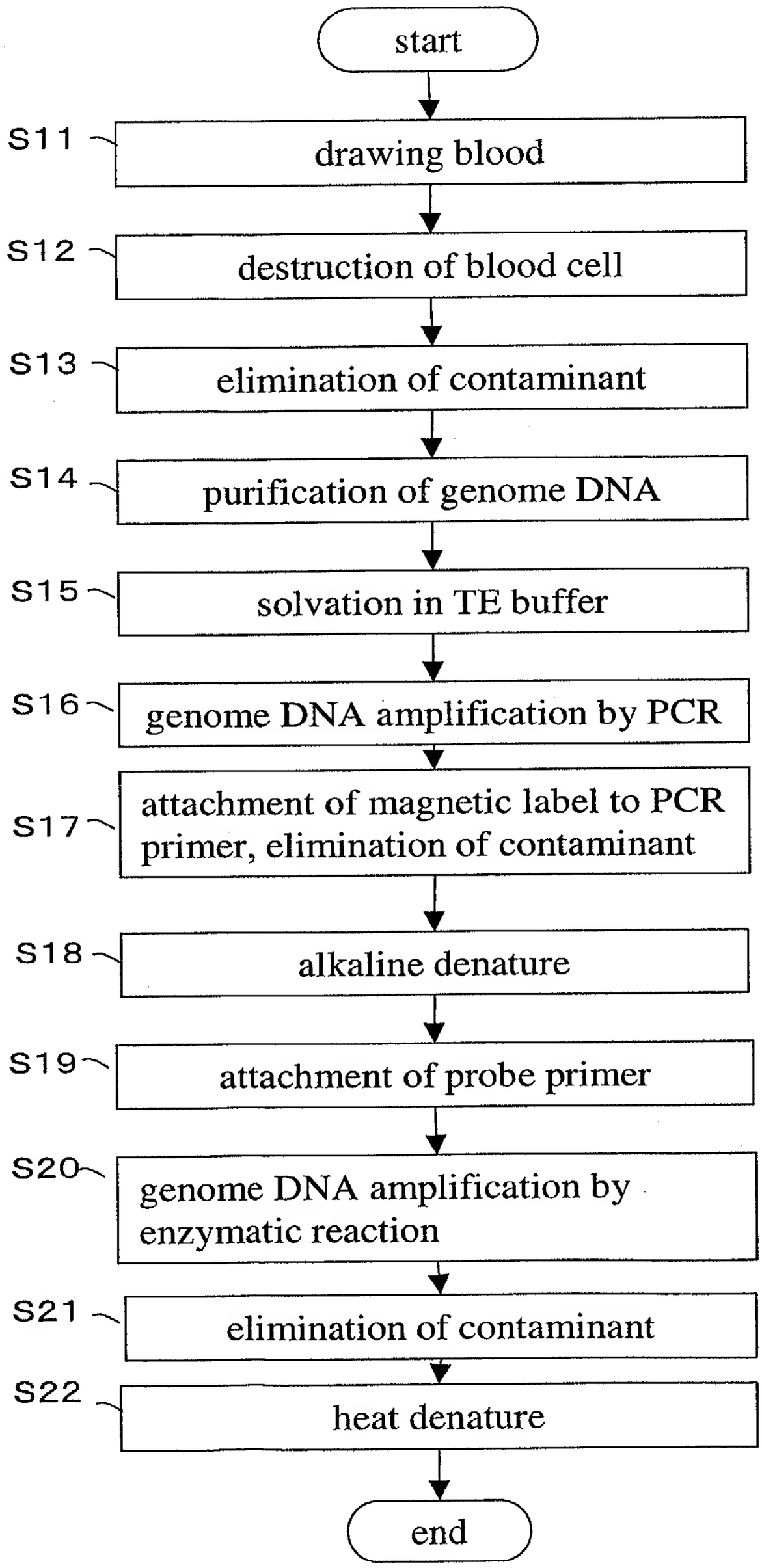

start
S11
drawing blood
S12
destruction of blood cell
S13
elimination of contaminant
S14
purification of genome DNA
S15
solvation in TE buffer
S16
genome DNA amplification by PCR
S17
attachment of magnetic label to PCR primer, elimination of contaminant
S18
alkaline denature
S19
attachment of probe primer
S20
genome DNA amplification by enzymatic reaction
S21
elimination of contaminant
S22
heat denature
end

Fig. 8

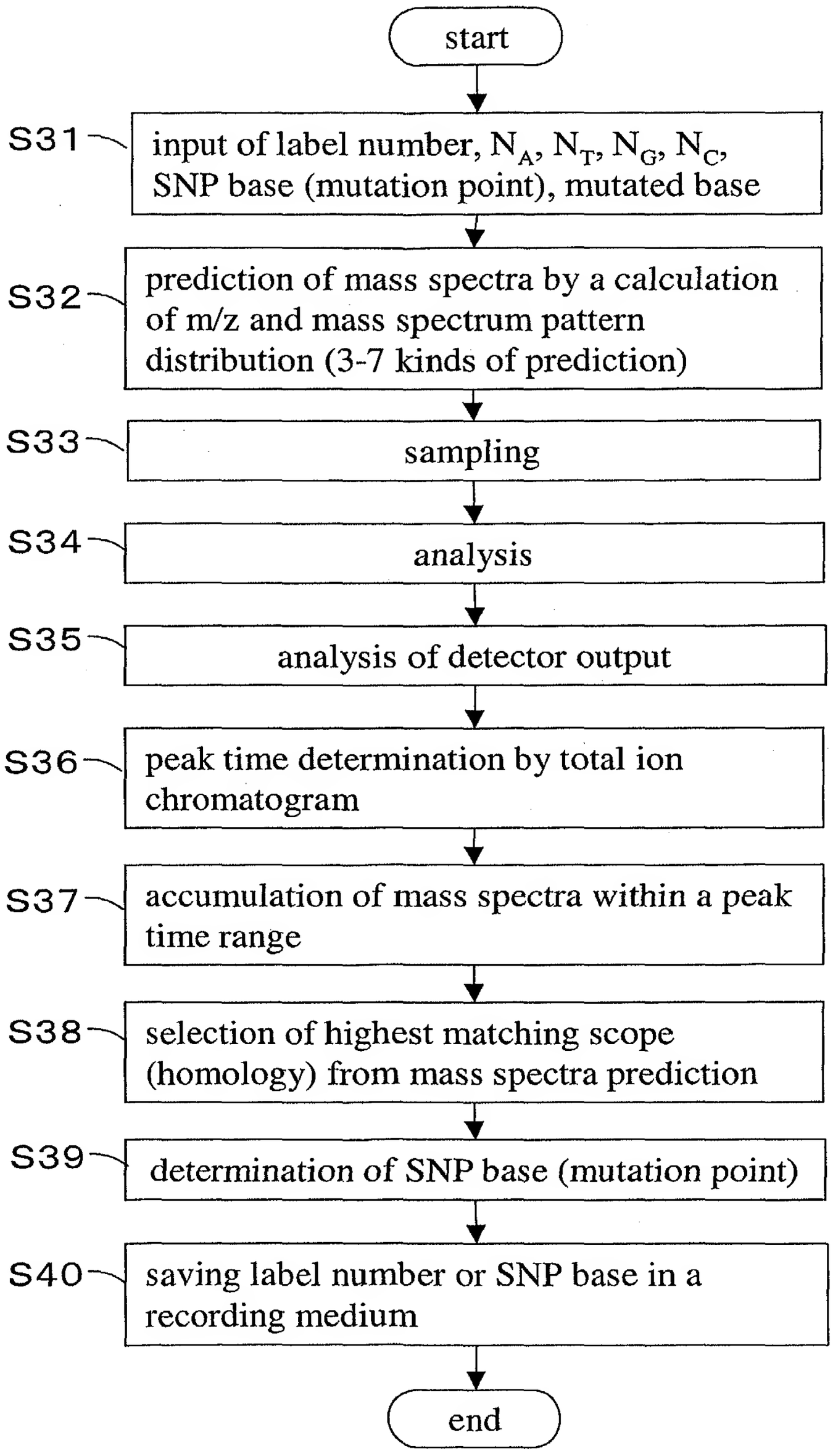

start
S31
input of label number, N_A, N_T, N_G, N_C, SNP base (mutation point), mutated base
S32
prediction of mass spectra by a calculation of m/z and mass spectrum pattern distribution (3-7 kinds of prediction)
S33
sampling
S34
analysis
S35
analysis of detector output
S36
peak time determination by total ion chromatogram
S37
accumulation of mass spectra within a peak time range
S38
selection of highest matching scope (homology) from mass spectra prediction
S39
determination of SNP base (mutation point)
S40
saving label number or SNP base in a recording medium
end

Fig. 9

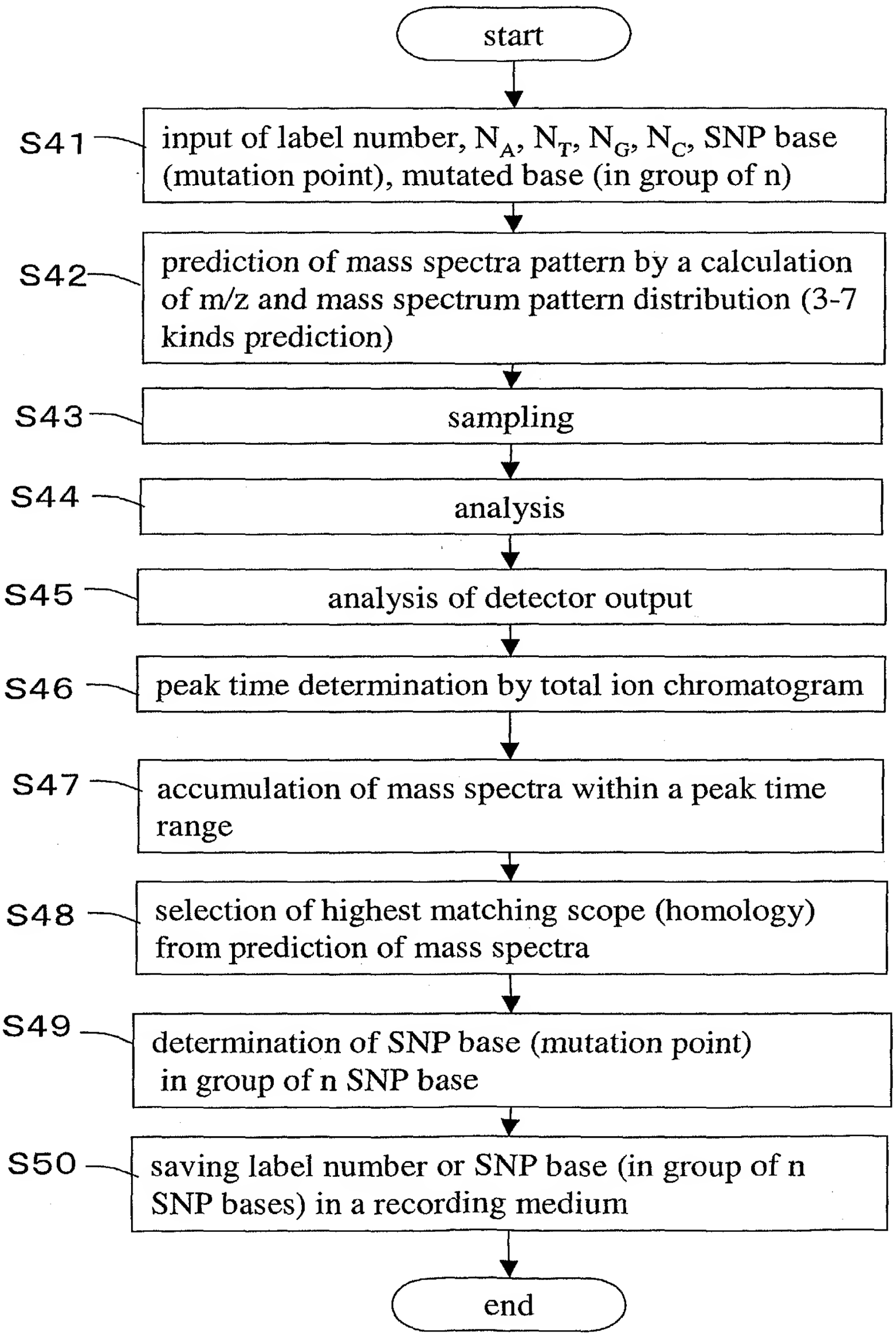

start
S41
input of label number, N_A, N_T, N_G, N_C, SNP base (mutation point), mutated base (in group of n)
S42
prediction of mass spectra pattern by a calculation of m/z and mass spectrum pattern distribution (3-7 kinds prediction)
S43
sampling
S44
analysis
S45
analysis of detector output
S46
peak time determination by total ion chromatogram
S47
accumulation of mass spectra within a peak time range
S48
selection of highest matching scope (homology) from prediction of mass spectra
S49
determination of SNP base (mutation point) in group of n SNP base
S50
saving label number or SNP base (in group of n SNP bases) in a recording medium
end

Fig. 10

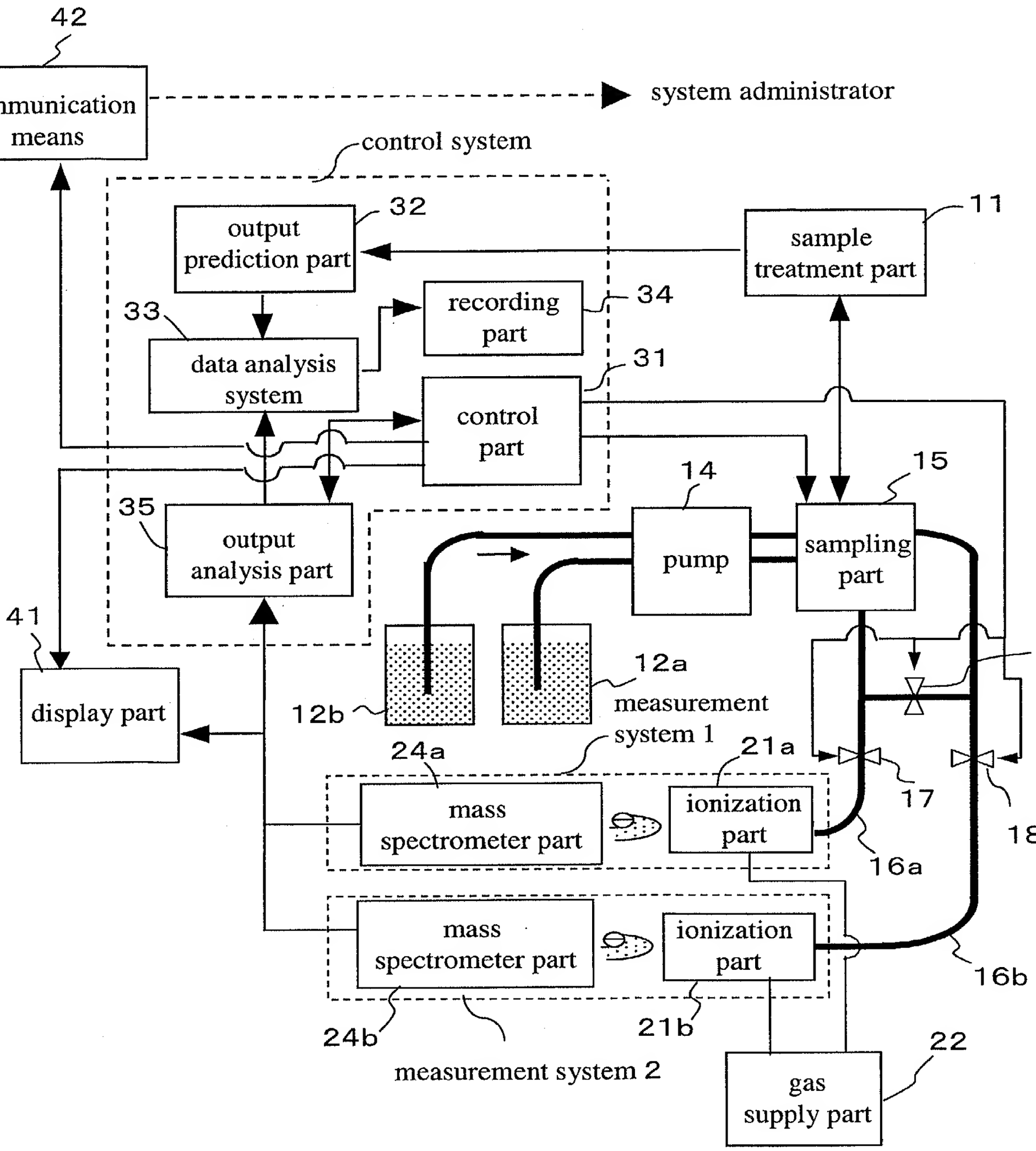

42
communication means
system administrator
control system
output prediction part
32
sample treatment part
11
recording part
34
33
data analysis system
31
control part
14
15
35
output analysis part
pump
sampling part
41
display part
12a
12b
measurement system 1
19
24a
21a
mass spectrometer part
ionization part
17
18
16a
mass spectrometer part
ionization part
16b
24b
21b
22
measurement system 2
gas supply part

Fig. 11

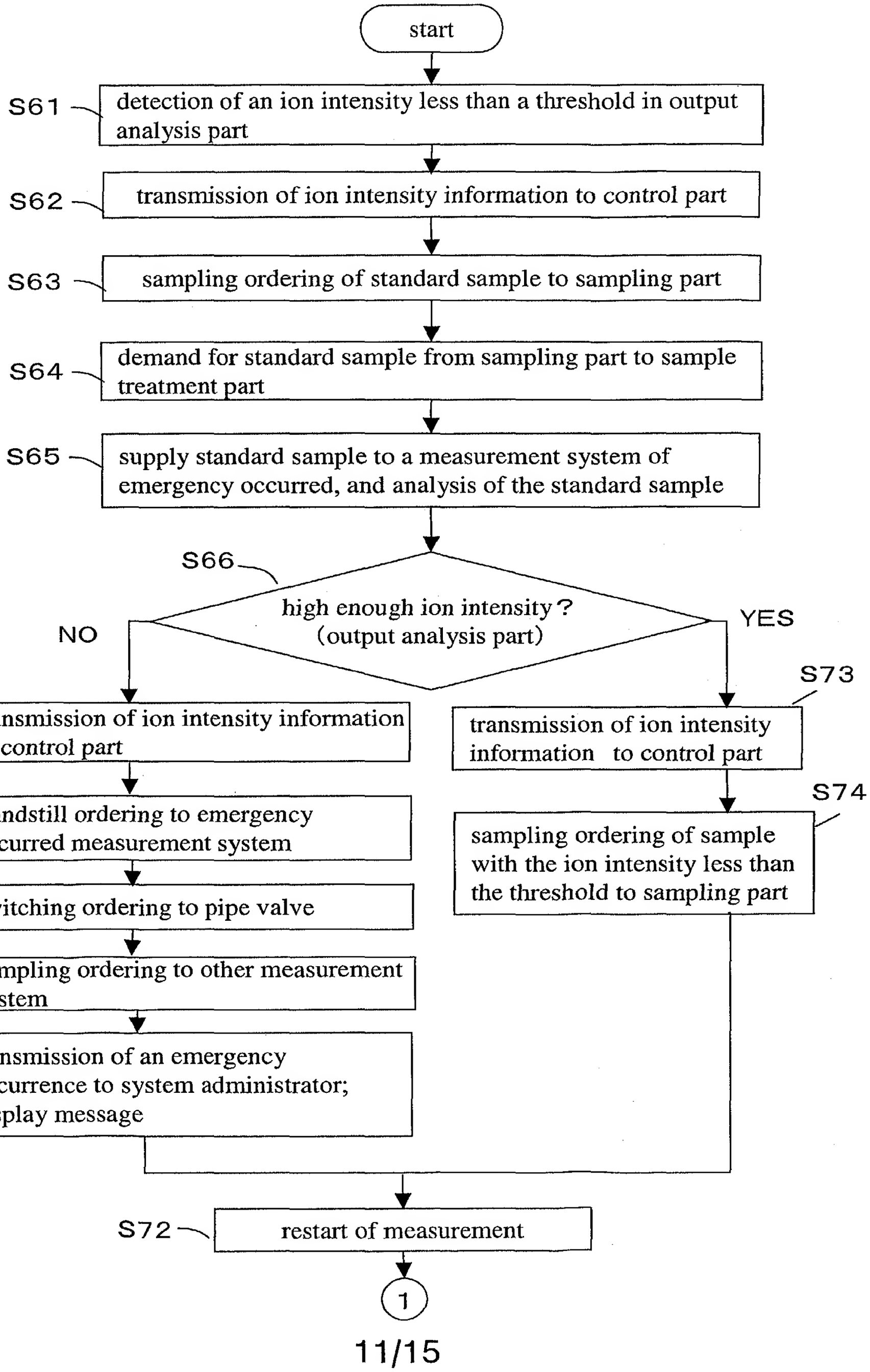

start
S61
detection of an ion intensity less than a threshold in output analysis part
S62
transmission of ion intensity information to control part
S63
sampling ordering of standard sample to sampling part
S64
demand for standard sample from sampling part to sample treatment part
S65
supply standard sample to a measurement system of emergency occurred, and analysis of the standard sample
S66
high enough ion intensity? (output analysis part)
NO
YES
S67
transmission of ion intensity information to control part
S68
standstill ordering to emergency occurred measurement system
S69
switching ordering to pipe valve
S70
sampling ordering to other measurement system
S71
transmission of an emergency occurrence to system administrator; display message
S73
transmission of ion intensity information to control part
S74
sampling ordering of sample with the ion intensity less than the threshold to sampling part
S72
restart of measurement
1

Fig. 12

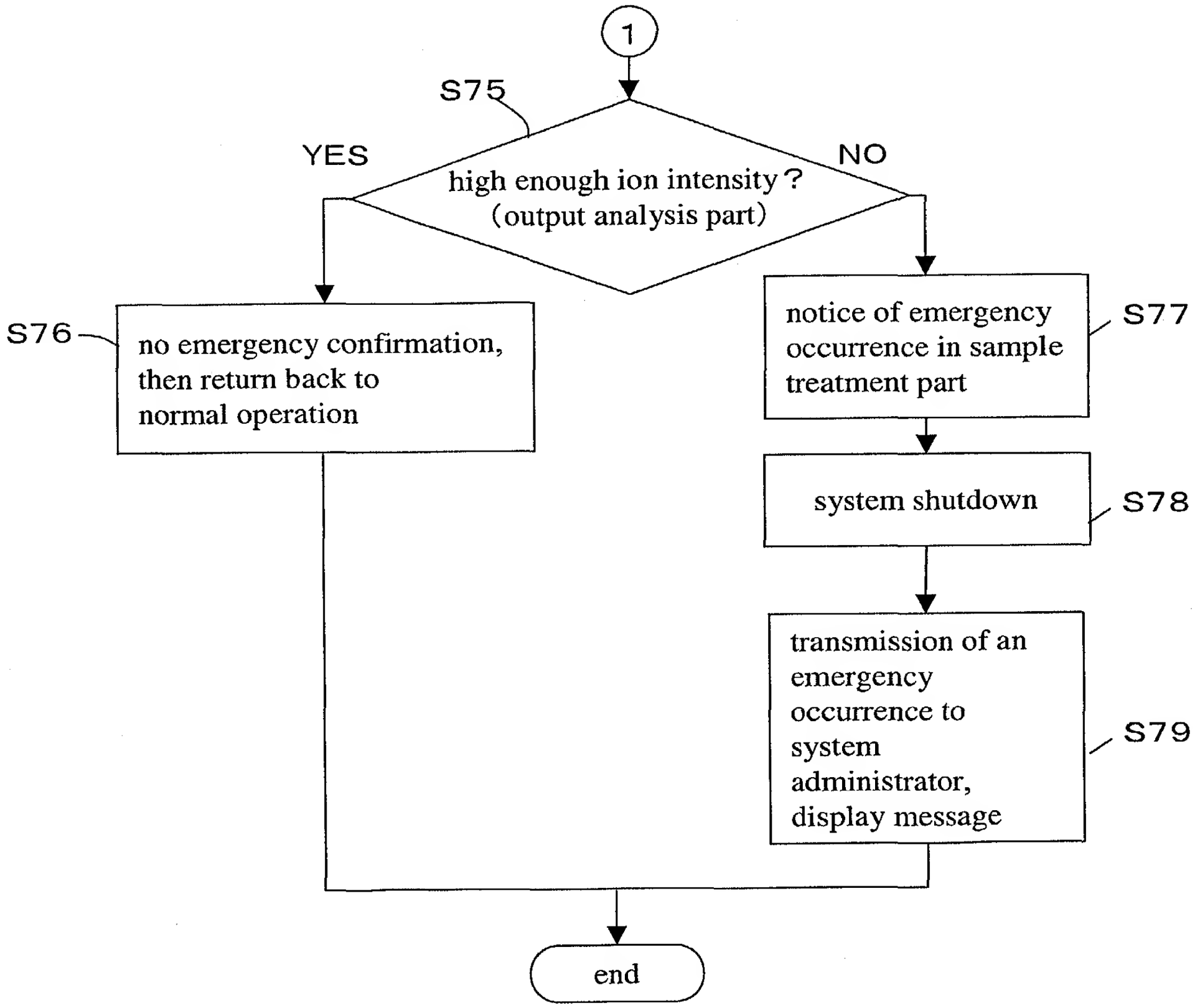
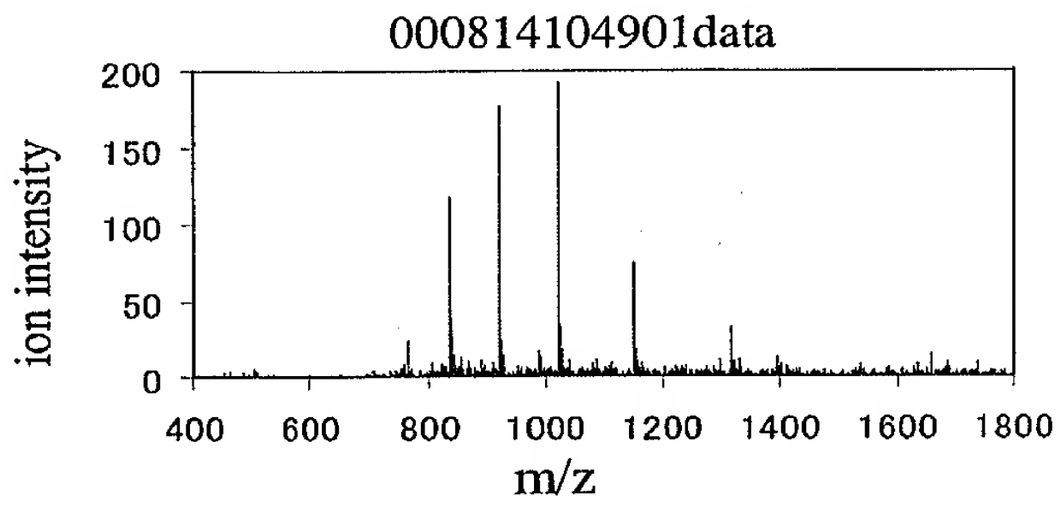

1
S75
YES
high enough ion intensity ?
(output analysis part)
NO
S76
no emergency confirmation, then return back to normal operation
notice of emergency occurrence in sample treatment part
S77
system shutdown
S78
transmission of an emergency occurrence to system administrator, display message
S79
end

Fig. 13

status of analysis:
normal

label number	base	notice
000814104853	A	
000814104854	A	
000814104855	A,T	
000814104856	A	
000814104857	A	
000814104858	A	
000814104859	T	
000814104900	A	
000814104901	A	



status of analysis:
emergency shutdown

label number	base	notice
000814104853	A	
000814104854	A	
000814104855	A,T	
000814104856	A	
000814104857	A	
000814104858	A	
000814104859	T	
000814104900	?	
############		standard sample

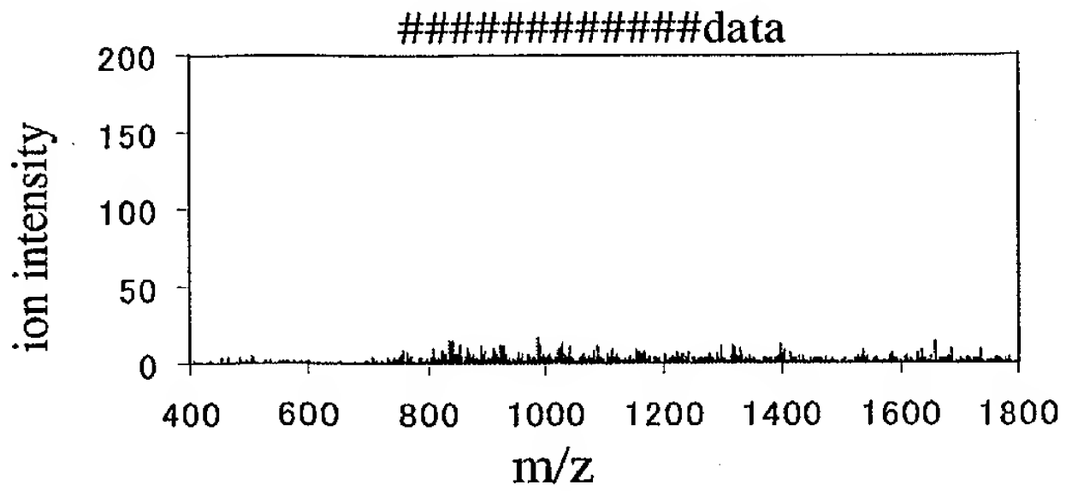


Fig. 14

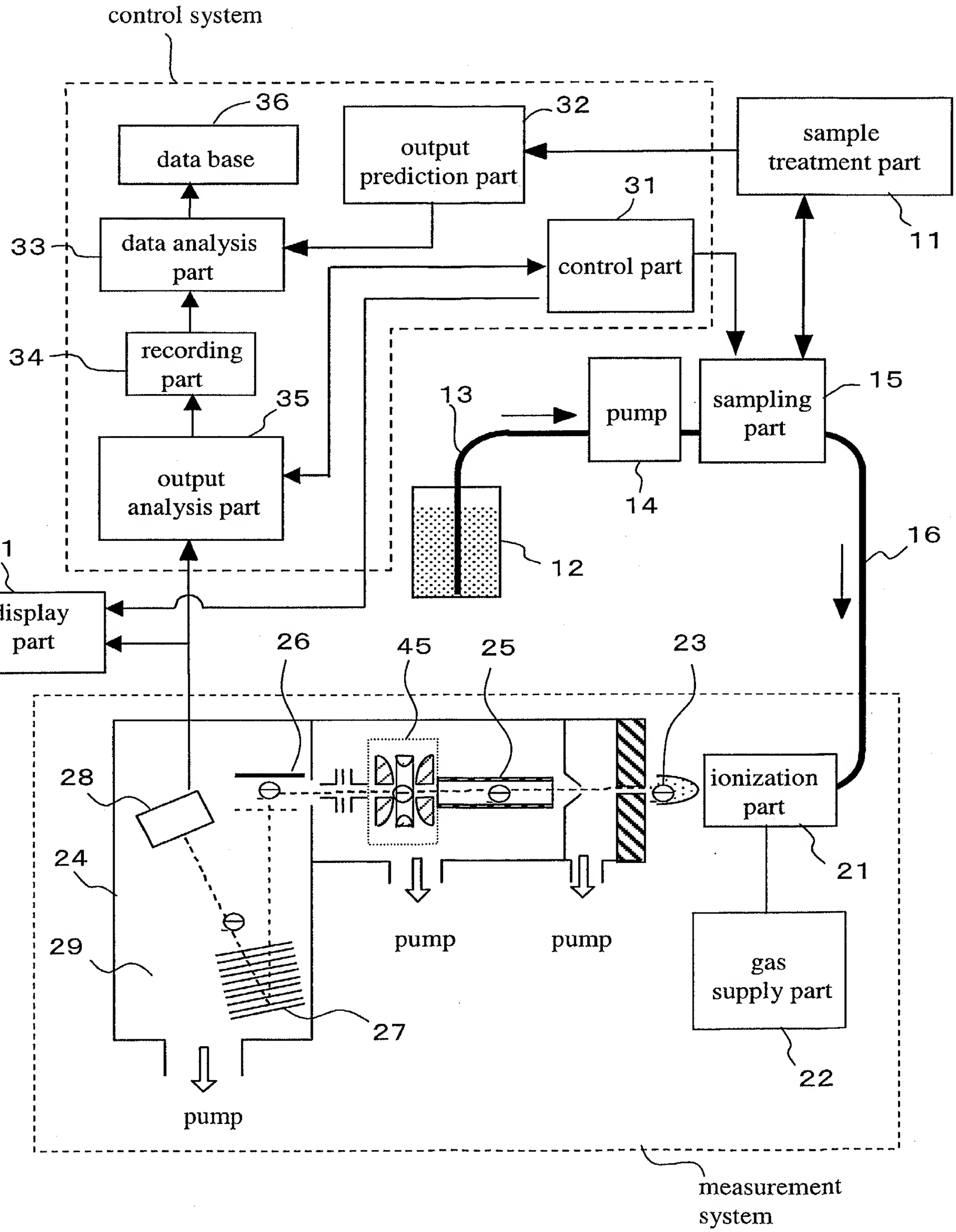
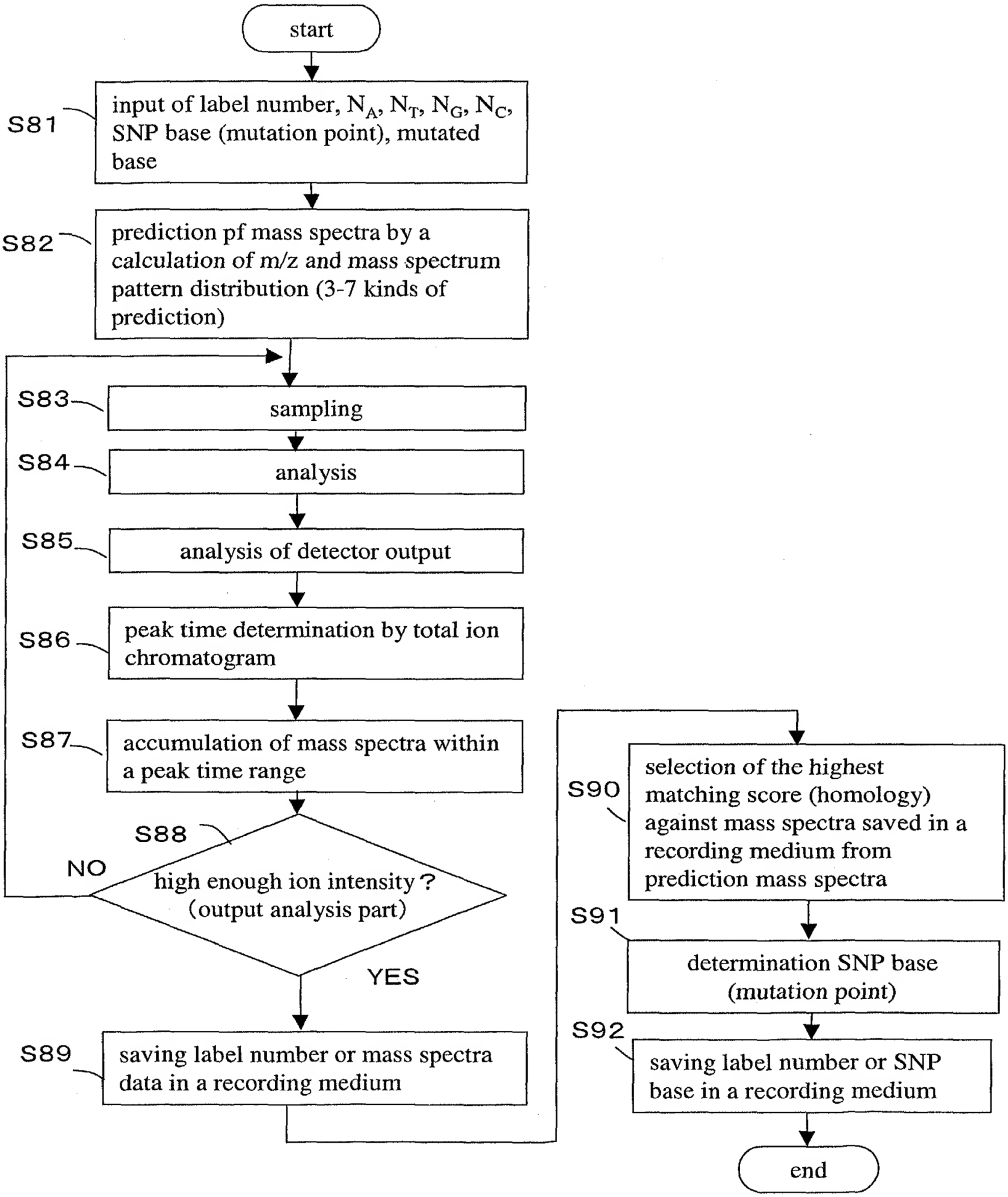

control system
36
data base
32
output prediction part
sample treatment part
11
31
33
data analysis part
control part
34
recording part
35
output analysis part
13
pump
15
sampling part
14
16
12
41
display part
26
45
25
23
28
ionization part
24
21
pump
pump
gas supply part
29
27
22
pump
measurement system

Fig. 15


start
S81
input of label number, N_A, N_T, N_G, N_C, SNP base (mutation point), mutated base
S82
prediction pf mass spectra by a calculation of m/z and mass spectrum pattern distribution (3-7 kinds of prediction)
S83
sampling
S84
analysis
S85
analysis of detector output
S86
peak time determination by total ion chromatogram
S87
accumulation of mass spectra within a peak time range
S88
high enough ion intensity ? (output analysis part)
NO
YES
S89
saving label number or mass spectra data in a recording medium
S90
selection of the highest matching score (homology) against mass spectra saved in a recording medium from prediction mass spectra
S91
determination SNP base (mutation point)
S92
saving label number or SNP base in a recording medium
end